



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 03:24 AM UTC

PDB ID : 3NS7 / pdb_00003ns7
Title : Succinic Acid Amides as P2-P3 Replacements for Inhibitors of Interleukin-1beta Converting Enzyme (ICE or Caspase 1)
Authors : Galatsis, P.
Deposited on : 2010-07-01
Resolution : 2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

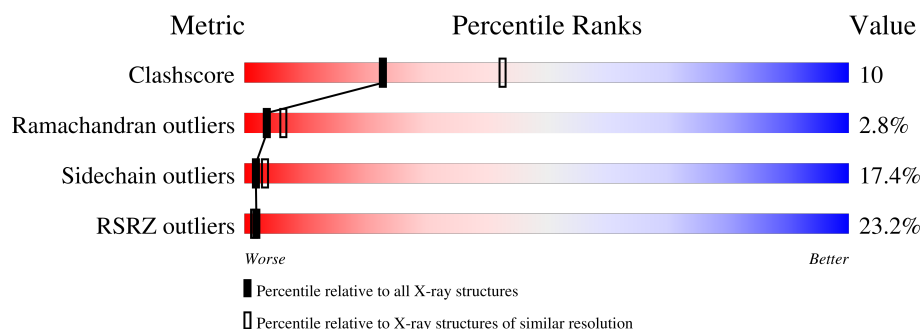
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	162	
2	B	88	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2073 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

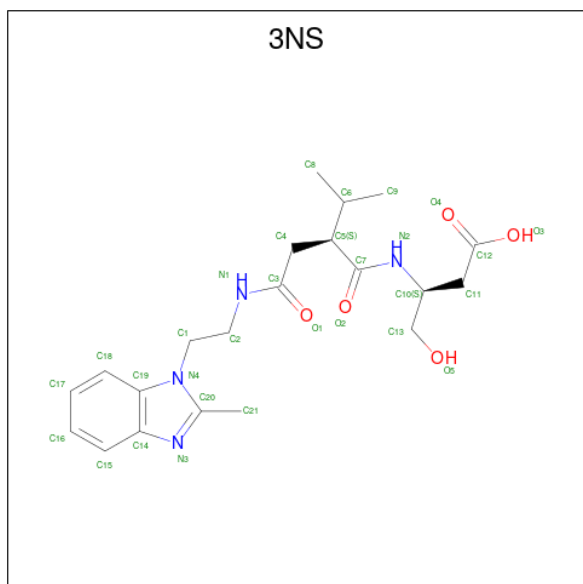
- Molecule 1 is a protein called Caspase-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	162	Total	C	N	O	S	1	0	0
			1277	801	222	243	11			

- Molecule 2 is a protein called Caspase-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	88	Total	C	N	O	S	0	0	0
			719	457	126	129	7			

- Molecule 3 is (3S)-4-hydroxy-3-{[(2S)-4-{[2-(2-methyl-1H-benzimidazol-1-yl)ethyl]amino}-2-(1-methylethyl)-4-oxobutanoyl]amino}butanoic acid (CCD ID: 3NS) (formula: C₂₁H₃₀N₄O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			30	21	4	5		

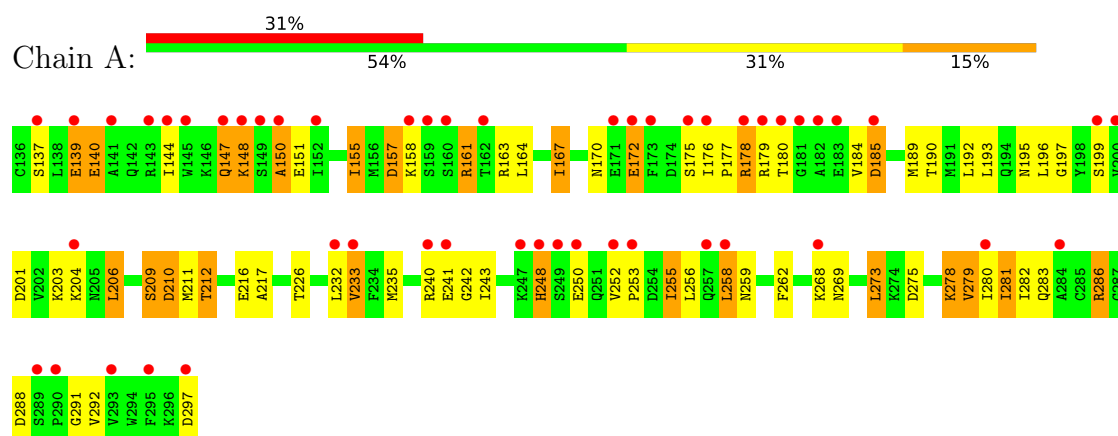
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	32	Total 32	O 32	0	0
4	B	15	Total 15	O 15	0	0

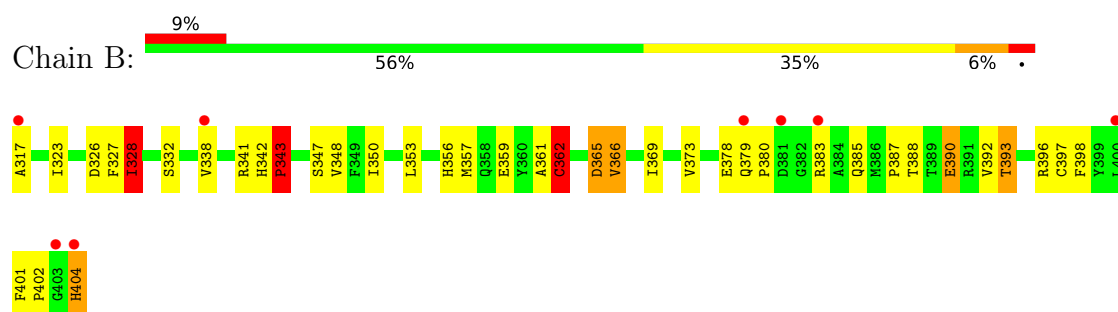
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Caspase-1



• Molecule 2: Caspase-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	63.95Å 63.95Å 158.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.60 25.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) (25.00-2.60) 97.3 (25.00-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.85 (at 2.60Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.188 , (Not available) 0.301 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	32.7	Xtriage
Anisotropy	0.349	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 40.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	2073	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.37% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 3NS

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.96	1/1299 (0.1%)	1.86	33/1749 (1.9%)
2	B	1.03	3/739 (0.4%)	1.88	20/995 (2.0%)
All	All	0.99	4/2038 (0.2%)	1.87	53/2744 (1.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
2	B	0	2
All	All	0	7

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	297	ASP	C-OXT	5.91	1.35	1.23
2	B	356	HIS	ND1-CE1	5.53	1.38	1.32
2	B	356	HIS	CE1-NE2	5.33	1.37	1.32
2	B	404	HIS	CE1-NE2	5.04	1.37	1.32

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	255	ILE	N-CA-C	8.82	120.63	107.75
2	B	343	PRO	CA-C-N	-7.53	110.60	122.65
2	B	343	PRO	C-N-CA	-7.53	110.60	122.65
1	A	292	VAL	N-CA-C	7.31	121.01	108.95
1	A	201	ASP	CA-C-N	-6.83	114.72	123.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	201	ASP	C-N-CA	-6.83	114.72	123.19
1	A	280	ILE	N-CA-C	6.77	120.81	113.43
1	A	151	GLU	CA-C-N	-6.75	112.96	122.34
1	A	151	GLU	C-N-CA	-6.75	112.96	122.34
2	B	338	VAL	N-CA-C	6.67	119.66	109.12
2	B	362	CYS	CA-C-N	-6.54	109.40	120.58
2	B	362	CYS	C-N-CA	-6.54	109.40	120.58
2	B	359	GLU	CA-C-N	-6.51	112.40	122.49
2	B	359	GLU	C-N-CA	-6.51	112.40	122.49
2	B	365	ASP	CA-CB-CG	-6.49	106.11	112.60
1	A	278	LYS	CA-C-N	-6.36	114.90	123.10
1	A	278	LYS	C-N-CA	-6.36	114.90	123.10
1	A	248	HIS	N-CA-C	6.27	119.30	109.96
1	A	288	ASP	CA-CB-CG	-6.21	106.39	112.60
2	B	317	ALA	CA-C-N	-6.07	114.85	123.10
2	B	317	ALA	C-N-CA	-6.07	114.85	123.10
1	A	211	MET	N-CA-C	5.99	117.50	110.97
2	B	366	VAL	N-CA-C	5.90	118.46	111.09
2	B	332	SER	N-CA-C	5.75	117.63	111.36
2	B	328	ILE	CA-C-N	-5.64	113.74	122.09
2	B	328	ILE	C-N-CA	-5.64	113.74	122.09
1	A	253	PRO	N-CA-C	5.61	119.69	110.55
1	A	232	LEU	CA-C-N	-5.60	115.16	122.94
1	A	232	LEU	C-N-CA	-5.60	115.16	122.94
1	A	189	MET	N-CA-C	5.57	117.35	111.28
1	A	281	ILE	N-CA-C	5.54	120.86	109.34
2	B	326	ASP	N-CA-C	5.54	119.86	113.38
2	B	378	GLU	N-CA-C	5.52	118.36	111.24
1	A	167	ILE	CA-C-N	-5.52	115.83	122.90
1	A	167	ILE	C-N-CA	-5.52	115.83	122.90
1	A	217	ALA	N-CA-C	5.49	117.26	111.28
1	A	242	GLY	N-CA-C	5.48	119.53	110.55
1	A	144	ILE	N-CA-C	5.46	115.66	110.42
1	A	185	ASP	CB-CA-C	-5.35	102.48	110.88
2	B	397	CYS	CA-C-N	-5.30	113.86	122.34
2	B	397	CYS	C-N-CA	-5.30	113.86	122.34
1	A	212	THR	CA-C-N	-5.30	112.77	120.29
1	A	212	THR	C-N-CA	-5.30	112.77	120.29
2	B	323	ILE	CA-C-N	-5.26	115.36	122.77
2	B	323	ILE	C-N-CA	-5.26	115.36	122.77
1	A	243	ILE	CA-C-N	-5.22	113.73	122.92
1	A	243	ILE	C-N-CA	-5.22	113.73	122.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	199	SER	CA-C-N	-5.13	116.03	123.11
1	A	199	SER	C-N-CA	-5.13	116.03	123.11
1	A	241	GLU	N-CA-C	5.13	116.95	111.36
1	A	280	ILE	N-CA-CB	-5.12	106.58	112.21
1	A	185	ASP	CA-CB-CG	5.03	117.62	112.60
1	A	161	ARG	N-CA-C	5.02	117.79	109.46

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	137	SER	Peptide
1	A	150	ALA	Peptide
1	A	178	ARG	Sidechain
1	A	240	ARG	Sidechain
1	A	291	GLY	Peptide
2	B	362	CYS	Peptide
2	B	396	ARG	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1277	0	1288	29	0
2	B	719	0	693	18	0
3	B	30	0	28	2	0
4	A	32	0	0	7	3
4	B	15	0	0	3	0
All	All	2073	0	2009	42	3

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (42) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:385:GLN:HA	4:B:15:HOH:O	1.31	1.28
1:A:158:LYS:HG2	4:A:41:HOH:O	1.67	0.93
1:A:258:LEU:HB2	4:A:7:HOH:O	1.71	0.89
1:A:206:LEU:HG	1:A:210:ASP:HB2	1.68	0.74
2:B:362:CYS:HB2	2:B:402:PRO:HD2	1.72	0.72
2:B:327:PHE:O	4:B:29:HOH:O	2.10	0.69
1:A:155:ILE:HD13	4:A:24:HOH:O	1.93	0.67
2:B:393:THR:N	4:B:29:HOH:O	2.24	0.65
1:A:273:LEU:HB3	1:A:278:LYS:HE3	1.79	0.63
1:A:163:ARG:HD2	1:A:197:GLY:O	1.98	0.63
2:B:383:ARG:HD3	3:B:1:3NS:C18	2.33	0.59
1:A:258:LEU:HD23	1:A:282:ILE:HD11	1.84	0.58
1:A:248:HIS:HA	1:A:252:VAL:O	2.05	0.56
1:A:148:LYS:NZ	4:A:6:HOH:O	2.38	0.56
1:A:157:ASP:O	1:A:161:ARG:HG3	2.06	0.56
1:A:258:LEU:CB	4:A:7:HOH:O	2.41	0.56
1:A:235:MET:HA	1:A:283:GLN:O	2.07	0.55
2:B:341:ARG:HA	2:B:347:SER:HA	1.89	0.53
1:A:286:ARG:HH22	2:B:390:GLU:CD	2.16	0.52
1:A:167:ILE:HA	1:A:233:VAL:HG13	1.92	0.51
1:A:155:ILE:HD11	2:B:398:PHE:HE2	1.77	0.50
1:A:170:ASN:O	1:A:179:ARG:HD3	2.14	0.48
1:A:268:LYS:HE3	1:A:269:ASN:OD1	2.15	0.47
2:B:357:MET:O	2:B:361:ALA:HB2	2.16	0.45
2:B:366:VAL:HG22	2:B:398:PHE:HB3	1.98	0.45
2:B:342:HIS:HA	2:B:343:PRO:HD2	1.87	0.45
1:A:161:ARG:HH12	2:B:404:HIS:C	2.24	0.45
1:A:176:ILE:HB	1:A:177:PRO:HD2	1.98	0.45
1:A:279:VAL:HB	2:B:328:ILE:HG23	1.99	0.45
1:A:155:ILE:CD1	4:A:24:HOH:O	2.57	0.44
1:A:172:GLU:CD	1:A:178:ARG:HH21	2.26	0.44
2:B:365:ASP:O	2:B:369:ILE:HG13	2.18	0.44
2:B:385:GLN:O	2:B:387:PRO:HD3	2.18	0.43
1:A:139:GLU:HA	4:A:47:HOH:O	2.19	0.43
1:A:185:ASP:HA	2:B:350:ILE:HG21	2.01	0.43
1:A:212:THR:O	1:A:216:GLU:HB2	2.20	0.42
1:A:204:LYS:O	1:A:206:LEU:HD13	2.19	0.41
1:A:139:GLU:HB2	1:A:140:GLU:H	1.74	0.41
1:A:147:GLN:HG2	1:A:148:LYS:HD3	2.02	0.41
2:B:379:GLN:HA	2:B:380:PRO:HD3	1.95	0.41
1:A:258:LEU:HD21	1:A:262:PHE:HE1	1.86	0.41
2:B:341:ARG:NH1	3:B:1:3NS:O2	2.55	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2:HOH:O	4:A:39:HOH:O[4_555]	0.37	1.83
4:A:1:HOH:O	4:A:45:HOH:O[6_455]	0.45	1.75
4:A:6:HOH:O	4:A:6:HOH:O[8_665]	1.97	0.23

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	160/162 (99%)	136 (85%)	20 (12%)	4 (2%)	4	8
2	B	86/88 (98%)	75 (87%)	8 (9%)	3 (4%)	3	4
All	All	246/250 (98%)	211 (86%)	28 (11%)	7 (3%)	4	6

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	281	ILE
1	A	140	GLU
1	A	209	SER
2	B	343	PRO
2	B	401	PHE
1	A	150	ALA
2	B	328	ILE

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	145/145 (100%)	115 (79%)	30 (21%)	1	2
2	B	79/79 (100%)	70 (89%)	9 (11%)	5	11
All	All	224/224 (100%)	185 (83%)	39 (17%)	2	3

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	139	GLU
1	A	147	GLN
1	A	148	LYS
1	A	155	ILE
1	A	157	ASP
1	A	164	LEU
1	A	172	GLU
1	A	175	SER
1	A	180	THR
1	A	184	VAL
1	A	190	THR
1	A	192	LEU
1	A	193	LEU
1	A	195	ASN
1	A	196	LEU
1	A	203	LYS
1	A	206	LEU
1	A	209	SER
1	A	210	ASP
1	A	226	THR
1	A	233	VAL
1	A	250	GLU
1	A	255	ILE
1	A	256	LEU
1	A	258	LEU
1	A	259	ASN
1	A	273	LEU
1	A	275	ASP
1	A	279	VAL
1	A	286	ARG
2	B	343	PRO
2	B	348	VAL
2	B	353	LEU
2	B	362	CYS
2	B	373	VAL

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Mol	Chain	Res	Type
2	B	388	THR
2	B	390	GLU
2	B	392	VAL
2	B	393	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	263	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	3NS	B	1	1	31,31,31	1.05	2 (6%)	38,42,42	1.30	6 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	3NS	B	1	1	-	9/28/28/28	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1	3NS	O3-C12	-2.96	1.21	1.30
3	B	1	3NS	C20-N3	2.23	1.34	1.31

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1	3NS	C18-C19-C14	-2.54	119.30	122.23
3	B	1	3NS	C4-C3-N1	-2.54	112.05	115.97
3	B	1	3NS	C19-C14-N3	-2.48	107.04	110.19
3	B	1	3NS	C14-C19-N4	2.36	107.42	105.55
3	B	1	3NS	C5-C7-N2	-2.26	113.28	116.01
3	B	1	3NS	O3-C12-C11	2.10	120.54	114.00

There are no chirality outliers.

All (9) torsion outliers are listed below:

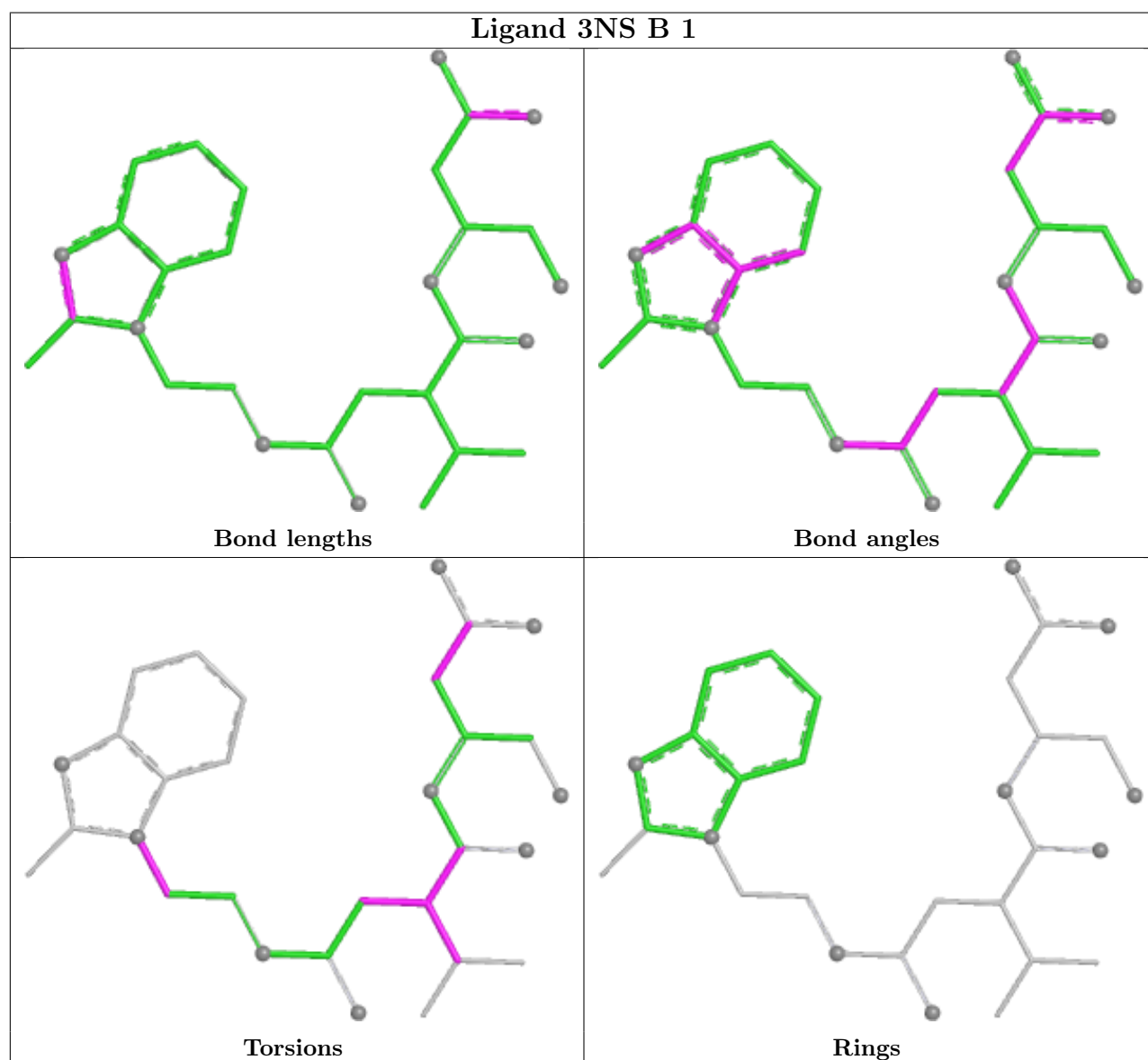
Mol	Chain	Res	Type	Atoms
3	B	1	3NS	C4-C5-C7-O2
3	B	1	3NS	C4-C5-C7-N2
3	B	1	3NS	C6-C5-C7-O2
3	B	1	3NS	C6-C5-C7-N2
3	B	1	3NS	C3-C4-C5-C6
3	B	1	3NS	C10-C11-C12-O3
3	B	1	3NS	C10-C11-C12-O4
3	B	1	3NS	C7-C5-C6-C9
3	B	1	3NS	C2-C1-N4-C19

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1	3NS	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	162/162 (100%)	1.66	50 (30%) 1 1	5, 22, 57, 83	1 (0%)
2	B	88/88 (100%)	1.15	8 (9%) 15 11	2, 15, 34, 55	0
All	All	250/250 (100%)	1.48	58 (23%) 2 1	2, 19, 53, 83	1 (0%)

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	139	GLU	6.0
1	A	241	GLU	5.6
1	A	148	LYS	5.5
2	B	403	GLY	4.6
1	A	252	VAL	4.5
1	A	250	GLU	4.4
2	B	381	ASP	4.4
1	A	172	GLU	4.3
1	A	145	TRP	4.2
2	B	379	GLN	4.2
1	A	147	GLN	4.1
1	A	185	ASP	3.8
1	A	183	GLU	3.7
1	A	160	SER	3.6
1	A	173	PHE	3.4
1	A	150	ALA	3.4
1	A	232	LEU	3.2
1	A	137	SER	3.2
1	A	257	GLN	3.1
1	A	159	SER	2.9
1	A	176	ILE	2.9
1	A	178	ARG	2.8
1	A	199	SER	2.8
1	A	253	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	149	SER	2.8
1	A	240	ARG	2.8
1	A	268	LYS	2.7
1	A	181	GLY	2.7
1	A	162	THR	2.7
1	A	182	ALA	2.6
1	A	175	SER	2.6
1	A	152	ILE	2.6
1	A	143	ARG	2.6
1	A	290	PRO	2.6
2	B	317	ALA	2.5
1	A	249	SER	2.5
1	A	297	ASP	2.5
1	A	180	THR	2.4
1	A	141	ALA	2.4
1	A	284	ALA	2.4
1	A	200	VAL	2.3
1	A	144	ILE	2.3
1	A	204	LYS	2.3
2	B	338	VAL	2.2
1	A	247	LYS	2.2
1	A	158	LYS	2.2
1	A	289	SER	2.2
1	A	258	LEU	2.1
1	A	280	ILE	2.1
1	A	295	PHE	2.1
1	A	171	GLU	2.1
2	B	404	HIS	2.1
1	A	293	VAL	2.1
1	A	179	ARG	2.1
2	B	400	LEU	2.0
2	B	383	ARG	2.0
1	A	248	HIS	2.0
1	A	233	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

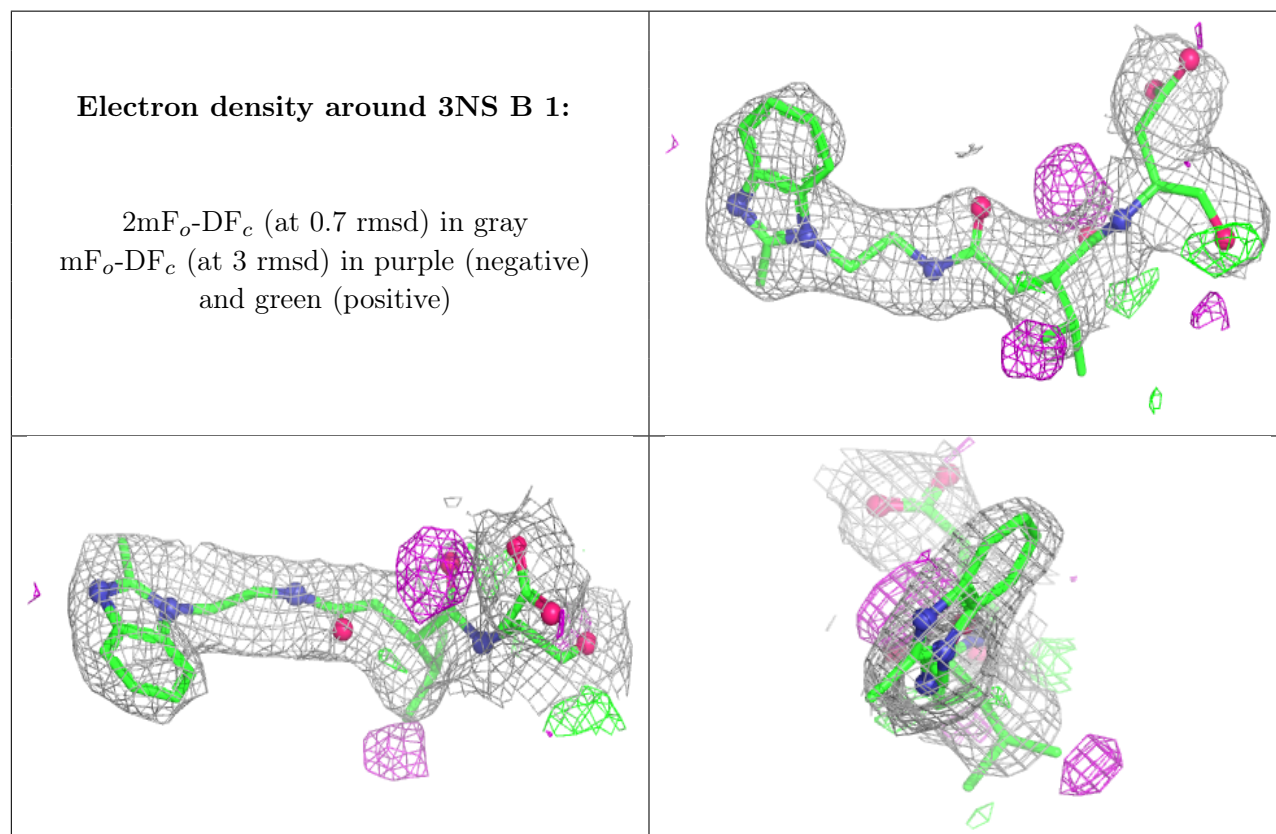
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	3NS	B	1	30/30	0.72	0.20	15,20,28,29	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.